

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2006, 09:26:06 ; Search time 0.001 Seconds
 (without alignments)
 143.112 Million cell updates/sec

Title: us-10-088-666-1
 Perfect score: 267
 Sequence: 1 tatatggaagtaagaccct.....agtagttgggggatcgcccc 267

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 0.5

Searched: 13 seqs, 268 residues

Total number of hits satisfying chosen parameters: 26

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 300 summaries

Database : rgedbl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result	Query						
No.	Score	Match	Length	DB	ID		Description
	1	25	9.4	25	1	AX105801	ACCESSION:AX105801
	2	25	9.4	25	1	AX105830	ACCESSION:AX105830
c	3	23	8.6	23	1	AX105781	ACCESSION:AX105781
	4	21	7.9	21	1	AX105749	ACCESSION:AX105749
	5	21	7.9	21	1	AX105827	ACCESSION:AX105827
	6	20	7.5	20	1	AR105913	ACCESSION:AR105913
	7	20	7.5	20	1	E04248	ACCESSION:E04248
	8	20	7.5	20	1	E07340	ACCESSION:E07340
	9	20	7.5	20	1	E07586	ACCESSION:E07586
	10	20	7.5	20	1	AX105802	ACCESSION:AX105802
	11	20	7.5	20	1	AX105826	ACCESSION:AX105826
c	12	18	6.7	18	1	AX105791	ACCESSION:AX105791
c	13	15	5.6	15	1	AR371336	ACCESSION:AR371336
c	14	11	4.1	21	1	AX105749	ACCESSION:AX105749
c	15	8.2	3.1	25	1	AX105801	ACCESSION:AX105801
c	16	7.8	2.9	25	1	AX105830	ACCESSION:AX105830
c	17	7.4	2.8	20	1	AX105802	ACCESSION:AX105802

c	18	7.2	2.7	20	1	AR105913	ACCESSION:AR105913
c	19	7.2	2.7	20	1	E04248	ACCESSION:E04248
c	20	7.2	2.7	20	1	E07340	ACCESSION:E07340
c	21	7.2	2.7	20	1	E07586	ACCESSION:E07586
c	22	7.2	2.7	21	1	AX105827	ACCESSION:AX105827
	23	6.8	2.5	23	1	AX105781	ACCESSION:AX105781
	24	6.2	2.3	15	1	AR371336	ACCESSION:AR371336
	25	6	2.2	18	1	AX105791	ACCESSION:AX105791
c	26	5.8	2.2	20	1	AX105826	ACCESSION:AX105826

OM nucleic - nucleic search, using sw model

Run on: October 12, 2006, 09:28:05 ; Search time 0.001 Seconds
 (without alignments)
 106.800 Million cell updates/sec

Title: us-10-088-666-1
 Perfect score: 267
 Sequence: 1 tatatggaagtaagaccct.....agtagttgggggatcgcccc 267

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 0.5

Searched: 8 seqs, 200 residues

Total number of hits satisfying chosen parameters: 16

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 300 summaries

Database : rnpbndbl:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query						Description
	No.	Score	Match	Length	DB	ID	
	1	25	9.4	25	1	US-11-348-413-350688	Sequence 350688,
	2	25	9.4	25	1	US-11-348-413-350689	Sequence 350689,
	3	25	9.4	25	1	US-11-348-413-988351	Sequence 988351,
	4	25	9.4	25	1	US-11-348-413-988352	Sequence 988352,
	5	25	9.4	25	1	US-11-348-413-988353	Sequence 988353,
	6	25	9.4	25	1	US-11-348-413-988354	Sequence 988354,
	7	25	9.4	25	1	US-11-348-413-988355	Sequence 988355,
	8	25	9.4	25	1	US-11-348-413-988356	Sequence 988356,
c	9	6.6	2.5	25	1	US-11-348-413-350688	Sequence 350688,
c	10	6.6	2.5	25	1	US-11-348-413-350689	Sequence 350689,
c	11	6.6	2.5	25	1	US-11-348-413-988352	Sequence 988352,
c	12	6.6	2.5	25	1	US-11-348-413-988353	Sequence 988353,
c	13	6.6	2.5	25	1	US-11-348-413-988354	Sequence 988354,
c	14	6.6	2.5	25	1	US-11-348-413-988355	Sequence 988355,
c	15	6.6	2.5	25	1	US-11-348-413-988356	Sequence 988356,
c	16	6.2	2.3	25	1	US-11-348-413-988351	Sequence 988351,

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OM nucleic - nucleic search, using sw model

Run on: October 12, 2006, 09:27:26 ; Search time 0.001 Seconds
(without alignments)
18.690 Million cell updates/sec

Title: us-10-088-666-1
Perfect score: 267
Sequence: 1 tatatggaagtaagaccct.....agtagttgggggatcgcccc 267

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 35 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : rnidb1:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	20	7.5	20	1	US-08-944-974A-1	Sequence 1, Appli
c	2	15	5.6	15	1	US-08-461-210-30	Sequence 30, Appl
c	3	7.2	2.7	20	1	US-08-944-974A-1	Sequence 1, Appli
	4	6.2	2.3	15	1	US-08-461-210-30	Sequence 30, Appl